We claim:

1. A transgenic expression constructs for predominant expression of a nucleic acid sequence of interest in substantially all vegetative plant tissues comprising a promoter sequence selected from the group consisting of

   a) the promoter of the *Pisum sativum* ptxA gene, functional equivalent fragments and functional equivalent homologs thereof, or their complements, having essentially the same promoter activity as the promoter of the *Pisum sativum* ptxA gene, and

   b) the promoter of the *Glycine max* extensin (SbHRGP3) gene, functional equivalent fragments and functional equivalent homologs thereof, or their complements, having essentially the same promoter activity as the promoter of the *Glycine max* extensin (SbHRGP3) gene,

   wherein said promoter sequence is operably linked to a nucleic acid sequence of interest to be transgenically expressed, and wherein said promoter sequence is heterologous with respect to said nucleic acid sequence of interest.

2. The transgenic expression construct of Claim 1, wherein the promoter sequence is selected from the group of sequences consisting of:

   a) the promoter of the *Pisum sativum* ptxA gene as described by SEQ ID NO: 1, or its complement,

   b) a functional equivalent fragment of at least 50 consecutive base pairs of the promoter sequence described by SEQ ID NO: 1, or its complement, having essentially the same promoter activity as the promoter sequence described by SEQ ID NO: 1,

   c) a functional equivalent homolog of the promoter sequence described by SEQ ID NO: 1 which has essentially the same promoter activity as the promoter sequence described by SEQ ID NO: 1, and has

      i) a homology of at least 95% over a sequence of at least 100 consecutive base pairs to the sequence as described by SEQ ID NO: 1 and/or

      ii) hybridizes under high stringency conditions with a fragment of at least 50 consecutive base pairs of the nucleic acid molecule described by SEQ ID NO: 1.

3. The transgenic expression construct of Claim 2, wherein the functional equivalent fragment comprises a sequence from about base pair 300 to about base pair 583 of the sequence described by SEQ ID NO: 1.

4. The transgenic expression construct of Claim 1, wherein the promoter sequence is selected from the group of sequences consisting of:

a) the promoter of the *Glycine max* extensin (SbHRGP3) gene as described by SEQ ID NO: 2, or its complement,

b) a functional equivalent fragment of at least 50 consecutive base pairs of the promoter sequence described by SEQ ID NO: 2, or its complement, having essentially the same promoter activity as the promoter sequence described by SEQ ID NO: 2,

c) a functional equivalent homolog of the promoter sequence described by SEQ ID NO: 2 which has essentially the same promoter activity as the promoter sequence described by SEQ ID NO: 2, and has

i) a homology of at least 60% over a sequence of at least 100 consecutive base pairs to the sequence as described by SEQ ID NO: 2 and/or

ii) hybridizes under high stringency conditions with a fragment of at least 50 consecutive base pairs of the nucleic acid molecule described by SEQ ID NO: 2.

5. The transgenic expression construct of Claim 4, wherein the functional equivalent fragment comprises a sequence from about base pair 800 to about base pair 1179 of the sequence described by SEQ ID NO: 2.

6. The transgenic expression construct of Claim 4, wherein the functional equivalent homolog is described by a sequence selected from group of sequences described by SEQ ID NO: 7, 8, and 9.

7. The transgenic expression construct of any of Claim 1 to 6, wherein the expression rate realized by the trangenic expression construct measured by an quantitative β-glucoronidase assay and normalized to units of β-glucoronidase per gram of biomass in seed and flower tissue is less the 10% of the corresponding value in total vegetative plant tissue.

8. The transgenic expression construct of Claim 1 to 7, wherein

a) the nucleic acid sequence of interest to be expressed is linked operably to further genetic control sequences, or

b) the expression construct comprises additional functional elements, or

c) both a) and b) apply.

9. The transgenic expression construct of Claim 1 to 8, wherein the nucleic acid sequence to be expressed transgenically results in,

a) expression of a protein encoded by said nucleic acid sequence, and/or

b) expression of sense, antisense, or double-stranded RNA encoded by said nucleic acid sequence.

10. The transgenic expression construct of Claim 1 to 9, wherein expression occurs in leafs, stems and roots but is not detectable in seeds.

11. A transgenic expression vector comprising a transgenic expression construct of any of Claim 1 to 10.

12. A non-human transgenic organism transformed with an expression construct as claimed in any of claims 1 to 10 or a vector as claimed in Claim 11.

13. The non-human transgenic organism of Claim 12, said organism selected from the group consisting of bacteria, yeasts, fungi, animal and plant organisms.

14. The transgenic organism of Claim 13 selected from the group consisting of sugarcane, maize, sorghum, pineapple, rice, barley, oat, wheat, rye, yam, onion, banana, coconut, date, hop, rapeseed, tobacco, tomato, tagetes (marigold), soybean, pea, common bean, and papaya.

15. A cell culture, part or transgenic propagation material derived from a transgenic organism of Claim 12 to 14.

16. A method for transgenic predominant expression of a nucleic acid sequence of interest in substantially all vegetative plant tissues comprising:

i. introduction of a transgenic expression construct into a plant cell or a plant, said transgenic expression construct comprising a promoter sequence selected from the group consisting of

a) the promoter of the *Pisum sativum* ptxA gene, functional equivalent fragments and functional equivalent homologs thereof, or their complements, having essentially the same promoter activity as the promoter of the *Pisum sativum* ptxA gene, and

b) the promoter of the *Glycine max* extensin (SbHRGP3) gene, functional equivalent fragments and functional equivalent homologs thereof, or their complements, having essentially the same promoter activity as the promoter of the *Glycine max* extensin (SbHRGP3) gene,

wherein said promoter sequence is operably linked to a nucleic acid sequence of interest to be transgenically expressed, and wherein said promoter sequence is heterologous with respect to said nucleic acid sequence of interest,

under conditions such that said nucleic acid sequence of interest is expressed in said plant cell and/or predominantly expressed in the vegetative plant tissue and/or organs of said transgenic plant.

17. The method of Claim 16, wherein expression occurs in leafs, stems and roots but is not detectable in seeds.

18. The method of Claim 16 or 17, said method further comprising one or more of the following steps
    ii) identifying or selecting the transgenic plant cell comprising said transgenic expression construct,
    iii) regenerating transgenic plant tissue from the transgenic plant cell,
    iv) regenerating a transgenic plant from the transgenic plant cell.

19. The method of any of Claim 16 to 18, wherein the transgenic expression construct is characterized as in Claim 1 to 10.

20. The use of a transgenic organism as claimed in claim 12 to 14 or of cell cultures, parts of transgenic propagation material derived therefrom as claimed in claim 15 for the production of foodstuffs, animal feeds, seeds, pharmaceuticals or fine chemicals.

21. A method for production of a foodstuff, animal feed, seed, pharmaceutical or fine chemical employing a transgenic organism as claimed in claim 12 to 14 or of cell cultures, parts of transgenic propagation material derived therefrom as claimed in claim 15.